

n.a. database search, using Smith-Waterman algorithm n.a. MPsrch\_nn

1357.154 Million cell updates/sec MasPar time 2402.20 Seconds Wed Jun 25 23:35:46 1997;

Title:

Tabular output not generated.

Run on:

>US-08-436-265-5 (1-2932) from US08436265.seq 2932

Description: Perfect Score: N.A. Sequence:

.....GCTTTATTTGCAAATCACCC 2932 .......CGAAATAAACGTTTAGTree 1 GCTCCGCGCCGAGGGCTGGA CGAGGCGCGCTCCCGACCT

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 .. STD Nmatch 333249 seqs, 550961234 bases x 2 Searched:

processing:

Listing first 45 summaries Minimum Match 0%

embl-newil Database:

1:BCT 2:FUN 3:GEN 4:HUM1 5:HUM2 6:HUM3 7:INV1 8:INV2 9:INV3 10:INV4 11:INV5 12:INV6 13:INV7 14:ORG 15:MAM 16:VRT 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC

23:VIR1 24:VIR2

genbank97 Database:

25.BCT1 26.BCT2 27.BCT3 28.BCT4 29.BCT5 30.BCT6 31.BCT7 32.BCT8 33.BCT9 34.GEN1 35.GEN2 36.HTG 37.INV1 38.INV2 45.INV4 41.INV5 42.INV6 43.INV7 44.INV8 45.INV9 46.MAN1 47.MAN3 49.VT1 50.VRT2 51.VRT3 52.PAT1 53.PAT2 54.PAT3 55.PAT4 56.PHG 57.PLN1 58.PLN2 59.PLN3 60.PLN4 61.PLN5 62.PLN6 63.PLN7 64.PLN8 65.PLN9 66.PLN10 67.PR11 68.PR12 69.PR13 70.PR14 71.PR15 72.PR16 73.PR17 74.PR18 75.PR12 76.PR13 70.PR14 71.PR15 72.PR16 73.PR17 74.PR18 75.PR19 77.PR11 78.PR112 79.PR113 80.PR114 81.ROD1 82.ROD2 83.ROD3 84.ROD4 85.ROD5 86.ROD6 87.ROD7 88.ROD8 89.STR 90.SYN 91.UNA 92.VRL1 93.VRL2 94.VRL3 95.VRL4 96.VRL5 97.VRL6 98.VRL7 99.VRL8 100.VRL9

genbank-new11 Database:

101:BCT 102:GEN 103:INV1 104:INV2 105:MAM 106:VRT 107:PHG 108:PLN 109:PR11 110:PR12 111:ROD 112:SYN 113:UNA 114:VRL

u-emb148 97

115:part1 1,16:part2

Mean 12.320; Variance 4.881; scale 2.524 "Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		Pred. No.	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	
		Description	H. sapiens ALK-3 mRNA.	bone morphogenetic pr	Mouse mRNA for BMP re	Mus musculus type I r	bone morphogenetic pr	Rat mRNA for bone mor	Rat mRNA for bone mor	M.musculus ALK-3 mRNA	Rat mRNA for bone mer	Mus musculus NIH3T3 t	Gallus gallus (clones	
		QI	HSALK3A	\$75359	MUSBMPRC	MMU04672	S74037	RATRALK3	<b>RNRALK3</b>	MMALK3A	RATRB4R1	MMU04673	CHKBRK1R	
		DB	70	88	84	82	20	87	20	81	87	82	49	
		Match Length DB	2932 70	3167	2292	2402	2620	3003	3003	1599	1599	2056	1969	
0/0	Query	Match	100.0	48.0	47.9	47.1	45.5	45.5	45.5	44.7	43.5	41.7	33.0	
		Score	2932	1408	1403	1380	1334	1334	1334	1311	1275	1223	296	
	Result	No.	1	7	m	4	S	9	7	80	σ	10	11	

ORGANISM Mus musculus

Query Match Resı Ю 1 GCTCCGCGCCGAGGCTGGA......GCTTTATTTGCAAATCACCC 2932 CGAGGCGCGGCTCCCGACT.......CGAAAAAAACGTTTAGTGGG 1 (bases 1 to 2292)
Suzuki, A., Thies, R.S., Yamaji, N., Song, J.J., Wozney, J., Murakami, K. .; Characterization and cloning of a putative receptor for BMP-2 and ъ, Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata, Vertebrata, Eutheria, Rodentia, Sciurognathi, Myomorpha, Muridae, Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; MasPar time 289.25 Seconds 937.757 Million cell updates/sec BRK-1; bone morphogenetic protein receptor kinase-1; full-length Submitted (22-DEC-1993) Jan S. Rosenbaum, The Procter & Gamble Company, Miami Valley Laboratories, P.O. Box 398707, Cincinnati, Koenig,B.B., Cook,J.S., Wolsing,D.H., Ting,J., Tiesman,J.P., Correa,P.E., Olson,C.A., Pecquet,A.L., Ventura,F., Grant,R.A., Chen,G., Wrana,J.L., Massague,J. and Rosenbaum,J.S. 17-SEP-1954 Gaps Gaps - n.a. database search, using Smith-Waterman algorithm Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; A truncated bone morphogenetic protein receptor affects . 9 C; Mismatches 214; Indels 11; Length 2402; dorsal-ventral patterning in the early Xenopus embryo Proc. Natl. Acad. Sci. U.S.A. 91, 10255-10259 (1994) Length 2292; Mus musculus type I receptor BPK-1 mRNA, complete cds. 0; Mismatches 180; Indels Score 1403; DB 84; Pred. No. 0.00e+00; DB 82; Score 1380; DB 82; Pred. No. 0.00e+00; BMP-4 from NIH3T3 cells Mol. Cell. Biol. 14, 5961-5974 (1994) 121476 segs, 46255616 bases x 2 Submitted (13-MAY-1993) to DDBJ by: Faculty of Pharmaceutical Sciences >US-08-436-265-5 (1-2932) from US08436265.seq Thu Jun 26 00:16:31 1997; mRNA receptor protein kinase. Query 0 Sapporo, Hokkaido 060 2402 bp 011-716-8513 011-716-8513 1 (bases 1 to 2402) 2 (bases 1 to 2402) 47.18; Best Local Similarity 88.2%; Best Local Similarity 89.6%; 1596; Conservative Matches 1683; Conservative TABLE default Gap 6 Direct Submission Tabular output not generated. 45239-8707, USA Rosenbaum, J.S. Dbase 0; Murinae; Mus. Murinae; Mus. Mus musculus house mouse and Kung, H. Naoto Ueno 2932 Gap 94344106 95024092 MMU04672 9538362 Phone: J04672 Japan Fax: n.a. •• Perfect Score: Sednence: Scoring table: Query Match Ery Match STD Description: DEFINITION ACCESSION ORGANISM TITLE JOURNAL Matches MPsrch nn AUTHORS Searched: MEDLINE REFERENCE REFERENCE AUTHORS JOURNAL MEDLINE REFERENCE AUTHORS JOURNAL KEYWORDS TITLE TITLE Run on: COMMENT Nmatch SOURCE Title: NID

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: n-geneseq26 1:part1 2:part2 3:pe

1.part1 2.part2 3.part3 4.part4 5.part5 6.part6 7.part7
8.part8 9.part9 10.part10 11.part11 12.part12 13.part13
14.part14 15.part15 16.part16 17.part17 18.part18
19.part19 20.part20 21.part21 22.part22 23.part23

Statistics: Mean 10.052; Variance 5.698; scale 1.764

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Pred. No.		sis; py; ss. useful peutic, en in d t t t he
Description	Human ALK-3 cDNA. Human Activin recepto Mouse Activin recepto BRK-1 DNA. Bone morphogenetic pr Mouse BMP type I rece Sequence encoding bon Truncated BRK-1. Mouse incomplete BMP Sequence encoding bon George 1 con the control of the	protein 1; morphogene receptor; gene thera receptor; gene thera relationship analogue - antagonists for thera antagonists for cateogenic s. The CDNAs are use in e.g. mammalian hos in vivo as a means o
ID	706031 Q66636 Q66640 Q90184 T27228 T27228 T28021 Q90183 T28027 Q83531	rrec rrec rrec rrec rrec rrec rrec rrec
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Length	2932 2932 2932 2402 2402 2402 2402 1613 1613 2056 2056 2056	(first entry)  inding receptor;  inding receptor;  ionist; antagonis  ionistic  ionisti
ery tch	100.0 99.7 47.1 47.1 47.1 44.2 44.2	standard; cDNA; 2932 BP L1996 (first entry) LK-3 cDNA. OP1 binding receptor; o gen; agonist; antagonist apiens. Location/Quali 3101908 aptide 310378 bp tide 3791905 c t= human ALK-3 103-A2. 1995; U05467. 1995; U05467. 1995; U05467. 1995; U05467. 1999; US-236428. CREATIVE BIOMOLECULES LUDWIG INST CANCER RES LUDWIG INST CANCER RES TY, Heldin C, Miyazano 1995; U05467. 1999; U05467. 1999; U05-236428. CREATIVE BIOMOLECULES LUDWIG INST CANCER RES TY, Heldin C, Miyazano 1995; U05467. 1999; U05-236428. CREATIVE BIOMOLECULES LUDWIG INST CANCER RES TY, Heldin C, Miyazano 1985; U05-67. 1997; U05-67. 1997; U05-67. 1998; U05-67. 1998; U05-67. 1998; U05-67. 1998; U05-67. 1998; U05-67. 1998; U05-67. 1999; U05-67. 1998; U05-67. 1998; U05-67. 1999; U05-67. 1990; U05-67. 19
Score	12932 12932 1380 1380 1223 1223 578	Tuent 1 Tuendard; cDNA; 2932 BP. Tuendard; cDNA; 2932 BP. Tuendard Tuendard Human ALK-3 cDNA. ALK-3; OP1 binding receptor; oster Morphogen; agonist; antagonist; of Homo sapiens. Location/Qualifie CDS Atag= b Attag= c Atag= b Attag= c Atag= b Attag= c Atag= c Arag= b Attag= c Arag= b Attag= c Atag= b Attag= c Atag= b Attag= c Atag= b Attag= c Atag= c Atag= b Attag= c Atag= c Atag= b Attag= c Atag= d Atag
sult No.	10 8 8 8 8 9 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1	SULT T0603: 13-FD1 Human ALK-3, morphe, Homo & Key CDS /*tag- /*tag- /*tag- /*tag- /*tag- /*tag- /*tag- //*tag- //tag- //tag-

DB 16; Length 2932;

Score 2932;

100.08;

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                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 29-32; 49pp; English.
S. CDNA library prepared from NIH3T3 poly-A RNA was screened with J159 PCR fragment to isolate clone BRK-1 (sequence given in Q90184) encoding full-length BMP receptor kinase protein (R74343)
                                                                                                                                                                                                                                                                           transforming growth factor, TGF, diagnostics, detection, therapy, rheumatoid arthritis, glome: "lar nephritis, fibrosis, ss.
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Human Activin receptor-like kinase 3 (hALK-3) cDNA
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Pred. No. 0.00e+00;
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Q66640 standard, cDNA, 2070
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Q66636 standard; cDNA; 2932
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Best Local Similarity 100.0%;
Matches 2932; Conservative
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2C18g04.rl Scares parathyroid tumor NbHPA Homo sapiens cDNA clone 322710 5' similar to gb:Z22535_cds1 SERINE/THREONINE-PROTEIN KINASE
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                                                                                         Minimum Match 0%
Listing first 45 summaries
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have specific binding affinity for
          osteogenic protein 1 (OP1) and OP1-related analogues.
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R85206, R85207 and R85209)
                                                               100.08;
                                                                        Best Local Similarity 100.0%;
                                                                                                                                                   (first entry)
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                                                                                   Matches 532; Conservative
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05-JUN-1995; US-462467.
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                                                                                                                                                                                                                                                  GB-024057
                                                                                                                                                                                                                                                                                   28-MAY-1993; GB-011647.
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                                                                                                                                                                                                                                                                                             02-JUL-1993; GB-013763
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30-OCT-1995; U14027.
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                                          532 AA;
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                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                    20-JAN-1995
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                                                                                                                                                                                                                     WO9411502-A.
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                                          Sequence
                                                               Query Match
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                                                                                                                                         R55368;
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3.26e-264
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1 MTQLYIYIRLLGAYLFIISR.....TALRIKKTLAKMVESQDVKI 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying osteogenic protein-1 receptor-binding analogue - useful in the design of morphogen agonists and antagonists for therapeutic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Type-I cell surface receptors ALK-2, ALK-3 and ALK-6 (given in
                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALK-3; OP1 binding receptor; osteogenic protein 1; morphogenesis;
                                                                                                                                                                                                                                                                                                                                                                                Bone morphogenic prot
Chick BMP type I rece
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                                                                                                                                                                                                                                                                                                                                                 Bone morphogenic prot
                                                                                                                                                                                                                   and is derived by analysis of the total score distribution.
                                                                                                                                                                         Mean 36.144; Variance 151.486; scale 0.239
                                                                                                                                                                                                                                                                                                                                                            Truncated BRK-1.
                                                                                                                                                                                                                                                                                                                             BRK-1 protein.
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                                                                                                                                                                                                                                                                                             Human ALK-3.
                                                                                                                                                                                                                                                                         Description
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                                                    92623 seqs, 10896596 residues
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/note= "serine/threonine-kinase domain"
                                                                                     summaries
                                                                                                                                                                                                                                        SUMMARIES
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Claim 1, Page 68-71, 95pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS.
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R74342
R85209
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(CREA-) CREATIVE BIOMOLECULES INC.
(LUDW-) LUDWIG INST CANCER RES.
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R95236
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K96201
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R85207 standard; Protein; 532 AA.
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                                                                                    Listing first 45
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Domain 153..235
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Domain 236..527
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532
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                     PAM 150
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N-PSDB; T06031.
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98.3
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                     Scoring table:
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Sequence:
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Gaps
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BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein.
                                                                                                                                                                                                                                                                                                                                                                                                   transforming growth factor; TGF; diagnostics; detection; therapy,
                                                                                                                                                                                                                                                                                                                                                                         serine threonine kinases; activin receptors; Act-R; superfamily;
receptors are used to identify novel morphogen receptor binding
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Length 532;
                                                                                                      Length 532
                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis; glomerular nephritis; fibrosis
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                                                                                                      Score 3981; DB 14;
Pred. No. 0.00e+00;
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3915; DB 13;
No. 0.00e+00;
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/label= Extracellular_ligand_binding_domain
Oomain 153..176
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                                                                                                                                                                                                                                    T 2
R55368 standard; Protein; 532 AA.
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R95225 standard; Protein; 532 AA
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                     analogues useful in drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES
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Domain 177..532
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23-NOV-1994; U13534.
24-NOV-1993; US-158735.
(PROC ) PROCTER & GAMBLE CO.
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in the design of morphogen agonists and antagonists for therapeutic, diagnostic and experimental purposes The Type-I cell surface receptors ALK-2, ALK-3 and ALK-6 (given R85206, R85207 and R85209) have specific binding affinity for osteogenic protein 1 (OP1) and OP1-related analogues. The receptors are used to identify novel morphogen receptor binding Identifying osteogenic protein-1 receptor-binding analogue Claim 1; Page 73-76; 95pp; English analogues useful in drug design. Heldin C, WPI; 95-393076/50. 502 AA; N-PSDB; T06032 ALTERNATE\_NAMES ORGANISM Perfect Score: Scoring table: Dijke PT, Score Seguence 3915 3900 3615 3139 2757 Query Match 3981 3981 2757 2747 1762 Description: m Statistics: Matches MPsrch\_pp Sednence: Searched: Database: Run on: No. Result RESULT ENTRY TITLE DATE ò ó, screening; reporter gene; bone morphogenetic protein-antagonist; Gaps bone morphogenetic protein receptor kinase-3; antibody; diagnostic; bone disorder; osteogenic; bone morphogenetic protein-agonist; Gaps Bone morphogenic protein, receptor; serine/threonine kinase; BMP; bone; cartilage; injury; treatment; inhibition. ALK-3; OP1 binding receptor; osteogenic protein 1; morphogenesis; ö ö Length 532; Indels Indels Mouse, bone morphogenetic protein receptor kinase-1; Bone morphogenetic protein type-I receptor kinase-1. 4 ; Score 3900; DB 13; Pred. No. 0.00e+00; Thies RS, Wozney JM, Yamaji N;A; Mismatches 10; Mismatches Bone morphogenic protein receptor CFKi-23a. /label= Intracellular\_domain /note= "serine/threonine-kinase domain" /note= "Peptide used to raise antibody" Location/Qualifiers Location/Qualifiers 09-NOV-1995. 28-APR-1995; U05467. 29-APR-1994; US-236428. (CREA-) CREATIVE BIOMOLECULES INC. . 9 285209 standard; Protein; 502 AA R70237 standard; Protein; 532 AA (LUDW-) LUDWIG INST CANCER RES. morphogen; agonist; antagonist /note= "Conserved BRK-1 motif" R96201 standard; Protein; 532 /label= Extracellular\_domain Jonain 123..205 /label= Transmembrane\_domain 98.0%; 97.2%; hormone-responsive element 28-SEP-1995 (first entry) 517; Conservative (first entry) (first entry) Conservative (GEMY ) GENETICS INST INC. (PROC ) PROCTER & GAMBLE ..497 216..221 23..122 04-NOV-1994; US-334179. 17-SEP-1993; US-123934. Rosenbaum JS . . 22 481 PIVSNRWNSDE 491 07-SEP-1994; U10080. 30-OCT-1995; U14085. Best Local Similarity /label= Sig\_peptide Rattus rattus WO9530003-AZ. W09614412-A2. 22-AUG-1996 Mus musculus 17-MAY-1996. 23-MAR-1995. Celeste AJ, WO9507982-A. 13-FEB-1996 522; Mouse ALK-6 Nohno T, Query Match Peptide Peptide Peptide R70237; R85209; R96201; Domain Domain ω Wus sp Domain drug Matches Matches Key Key RESULT
ID R7
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protein - protein database search, using Smith-Waterman algorithm
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                                 Gaps
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03-0ct-1995 #sequence_revision 03-0ct-1995 #text_change
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Score 2757; DB 14; Length 502; Pred. No. 3.26e-264;
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                                76; Mismatches 61; Indels
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 69.3%;
                Best Local Similarity 71.9%;
                                363; Conservative
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                                                                                                                             Tabular output not generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5027
                                                                                                                                                                                                                                             PAM 150
                                                                                                                                                                                                                                                             Gap 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A56238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0
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78.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.3
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5.

Sampath KT;

Miyazano K,

Qy         121 TIECCRTNLCNQYLQPTLPPVVIGBFFDGSIRWLVLLISMAVCIIAMIFFSSCFCYKHYC         180           Db         181 ksissrgrynrdleqdeafipvgeslkdlidqsqssgsgsplpllvqrtiakqiqmvrqv         240           Cl	Db 361 rdlksknilikkngscciačiglavkfnsdtnevdiplntrvgtkryman	Run on: Tabular output n Title: Description: Perfect Score: Sequence: Scoring table: Searched: Post-processing:	ase: swiss-prot34  1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part  8:part9 9:part9 10:part10 11:part11  stics: Mean 50.780; Variance 83.714; scale 0.607  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printe and is derived by analysis of the total score distribution.  SUMMARIES  *  Query	No. Score Match Length DB 1D Description Pred. No. 1 3981 100.0 532 5 KIR5 HUMAN SERINE/THREONINE-PROT 0.00e+00 2 3915 99.3 532 5 KIR5 MOUSE SERINE/THREONINE-PROT 0.00e+00 4 2747 69.0 502 5 KIR6 MOUSE SERINE/THREONINE-PROT 0.00e+00 5 1762 44.3 503 5 KIR4 HUMAN SERINE/THREONINE-PROT 0.00e+00 6 1737 43.6 501 5 KIR4 HUMAN SERINE/THREONINE-PROT 0.00e+00 7 1638 41.1 509 5 KIR1 HUMAN SERINE/THREONINE-PROT 0.00e+00 8 1630 40.9 509 5 KIR1 HUMAN SERINE/THREONINE-PROT 0.00e+00 9 1617 40.6 509 5 KIR1 HUMAN SERINE/THREONINE-PROT 0.00e+00 1614 40.5 505 5 KIR2 HUMAN SERINE/THREONINE-PROT 0.00e+00 0.00e+0
IONS A56238; S40158; I48242; I49543  NCE  Chors A56238  Chors A56238  Chors B.B.; Cook, J.S.; Wolsing, D.H.; Ting, J.; Tiesman, J.P.; Correa, P.E.; Olson, C.A.; Pecquet, A.L.; Ventura, F.; Grant, R.A.; Chen, G.X.; Wrana, J.L.; Massague, J.; Rosenbaum, J.S. (1994) 14:5961-5974  Characterization and cloning of a receptor for BMP-2 and BMP-4 from NIH 3T3 cells.  Cession A56238  ##status  ##molecule_type mRNA  ##residues  1-532 ##label KOE  ##cross-references GB:U04672  AANTE CASS-references GB:U04672	0 0 0 H	Din Din Ita	e le	Local Similarity 98.1%; Pred. No. 0.00e+00; hes 522; Conservative 6; Mismatches 4; Indels 0; Gaps 0; mtqlytyirllgaclfiishvqqqnldsmlhqtgmksdldqkkpengvtlapedtlpflk 60
ACCESSIONS REFERENCE #authors #journal #fitle #accession #status #molecule ##residues ##residues ##residues	#authors #authors #authors #submission #accession #staus ##staus ##molecule ##residues ##residues ##residues	#journal #title #cross_refere #accession ##status ##molecule ##residues ##rcross_re REFERENCE #authors #journal #title #cross_refere		Best Local S.     Matches   52     Db

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PROSITE; PS00108; PROTEIN_KINASE_ST.
PROSITE; PS50011; PROTEIN_KINASE_DOM.
RECEPPOR; TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00107; PROTEIN KINASE ATP.
PROSITE; PS00108; PROTEIN KINASE ST.
PROSITE; PS50011; PROTEIN KINASE DOM.
RECEPTOR; TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;
TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL.
                                                                                                                                                                                                                                                                                                      SERINE/THREONINE-PROTEIN KINASE RECEPTOR R6 PRECURSOR (EC 2.7.1.37)
  -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES. STRONG, TO ACTIVIN RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES. STRONG, TO ACTIVIN RECEPTORS.
                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                TEN DIJKE P., YAMASHITA H., ICHIJO H., FRANZEN P., LAIHO M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                   (SKR6) (ACTIVIN RECEPTOR-LIKE KINASE 6) (ALK-6)
                                                                                                                                                                                                                                                           01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
                                                                               PROSITE; PS00107; PROTEIN_KINASE_ST.
                                                                                                                                       TRANSMEMBRANE; GLYCOPROTEIN; SIGNAL
                                                                                                                                                                 Best Local Similarity 98.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SCIENCE 264:101-104(1994).
                                                                                                                                                                              522; Conservative
                                                      EMBL; U04672; G538363; -.
                                                                                                                                                                                                                                                                                                                                                                                                                           MIYAZONO K., HELDIN C.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z23143; G437871; -.
                                          EMBL; D16250; G577634; -.
                                                                                                                                                                                                                                    STANDARD;
                             EMBL; Z23154; G437869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A53444; A53444.
PIR; S40159; S40159.
                                                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE)
                                                                    PIR; S40158; S40158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14
127
149
204
210
231
332
502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P01359; 1PCP.
                                                                                                                                                                                                                                                                                                                                                            EUTHERIA; RODENTIA
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 94188705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2932
                                                                                                                                                                                                                                   KIR6 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.A. Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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BINDING
                                                                                                                                                                                                                                                 P36898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                              Matches
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   ó
                                        1.21e-171
3.66e-169
3.39e-165
                                                                                 3.39e-165
                                                                                               1.88e-164
                                                                                                            1.02e-162
               0.00e+00
                             0.00e+00
  0.00e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUZUKI A., THIES R.S., YAMAJI N., SONG J.J., WOZNEY J., MURAKAMI K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
SERINE/THREONINE-PROTEIN KINASE RECEPTOR R5 PRECURSOR (EC 2.7.1.37)
                                                                                                                                                                                                        01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
SERINE/THREONINE-PROTEIN KINASE RECEPTOR R5 PRECURSOR (EC 2.7.1.37)
(SKRS) (ACTIVIN RECEPTOR-LIKE KINASE 3) (ALK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 94344106.
KOENIG B.B., COOK J.S., WOLSING D.H., TING J., TIESMAN J.P., CORRAP P.E., OLSON C.A., PECQUET A.L., VENTURA F., GRANT R.A., CHEN G., WRANA J.L., MASSAGUE J., ROSENBAUM J.S.; MOL. CELL. BIOL. 14:5561-5974 (1994).

-!- FUNCTION: RECEPTOR FOR BMP-2 AND BMP-4.

-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA
                                                                                 TYPE
               SERINE/THREONINE-PROT
                                          ACTIVIN RECEPTOR TYPE
                                                      CELL-SURFACE RECEPTOR
                                                                    ACTIVIN RECEPTOR TYPE
                                                                                               ACTIVIN RECEPTOR TYPE
                                                                                                            PUTATIVE SERINE/THREO
                                                                                                                        ACTIVIN RECEPTOR TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SKRS) (ALK-3) (BMP-2/BMP-4 RECEPTOR).
                             SERINE/THREONINE-PROT
   SERINE/THREONINE-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 3981; DB 5; Length 532;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                     TEN DIJKE P., ICHIJO H., FRANZEN P., SCHULZ P., SARAS J., TOYOSHIMA H., HELDIN C.H., MIYAZONO K.; ONCOGENE '8:2879-2887 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                 ACTIVIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIYAZONO K., MOREN A., GRIMSBY S., ICHIJO H., HELDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (JUN-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROC. NATL. ACAD. SCI. U.S.A. 91:10255-10259(1994)
                                                                                                                                                                 532 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 AA
             KIR3_HUMAN
KIR3_RAT
AVR2_XENLA
DAF1_CAEEL
                                                                                              AVR2_RAT
YQD2_CAEEL
AVRB_XENLA
                                                                                 AVR2 MOUSE
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                            01-JUN-1994 (REL. 29, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (REL. 29, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
                                       514 1
669 3
513 1
513 1
513 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     532; Conservative
                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                            HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUTHERIA, RODENTIA.
                                                                                                                                                                                                                                                                                                      EUTHERIA; PRIMATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=BRAIN;
MEDLINE; 95024092
                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 93390967
                                                                                                                                                                                                                                                                                                                                              TISSUE=PLACENTA;
              37.9
                                          21.4
21.2
20.7
20.7
20.7
20.7
20.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=SWISS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TEN DIJKE P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIRS MOUSE
P36895;
                                                                                                                                                      T 1
KIRS HUMAN
1612
1509
1498
852
842
826
826
826
826
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                                                                                                                                                                              P36894;
                                                                                                                                                                                                                                                               ACVRLK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACVRLK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
    111
122
124
125
126
129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                    RESULT
                                                                                                                                                                              OC OS OS OC
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Gaps

0

Length 532;

Score 3915; DB 5; Pred. No. 0.00e+00;

98.3%;

6; Mismatches

502 AA

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GCTCCGCGCCGAGGGCTGGA......GCTTTATTTGCAAATCACCC 2932
                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                           851.271 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                            n.a. - n.a. database search, using Smith-Waterman algorithm
                                                                                                                                                                                                                                                                            Sat May 24 07:04:02 1997; MasPar time 98.46 Seconds
                                                                                                                                                                                                          'n.
                                                                                                                                                                       Score 2757; DB 5; Length 502; Pred. No. 0.00e+00;
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                        76; Mismatches 61;
                                                                                  ATP (BY SIMILARITY)
ATP (BY SIMILARITY)
                                                                                                                                      56944 MW; D1EC67A0 CRC32;
                                                                   PROTEIN KINASE
                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                              >US-08-436-265-5
(1-2932) from US08436265.seq
                                                                                                                      ΒY
                                                                                                                                                                       69.3%;
                                                                                                                                                                                       71.9%;
                                                                                                                                                                                                          363; Conservative
                                                                                                                                                                                                                                                                                                            Tabular output not generated.
502
126
148
502
494
                                                                                  218
                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  _
                                                                                                                                                                                                                                                                                                                                                                                                                Comp:
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SERINE/THREONINE KINASE RECEPTOR R6

POTENTIAL.

EXTRACELLULAR (POTENTIAL) POTENTIAL. CYTOPLASMIC (POTENTIAL)

protein - protein database search, using Smith-Waterman algorithm MasPar time 5.02 Seconds 348.411 Million cell updates/sec 1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prin and is derived by analysis of the total score distribution. .....TALRIKKTLAKMVESQDVKI MORPHOGENIC PROTEIN-SPECIFIC CELL SURFACE RECEPTORS AND USES THEREFOR Mean 9.515; Variance 4.793; scale 1.985 Sequence 1, Sequence 1, Sequence 3, Sequence 2, Sequence 2, Sequence 2, Sequence 7, Sequence 6, Sequen Sequence 4, Description BP × PCT-US95-05467-5 STANDARD; DNA; UNC; 2932 10:PCT94 11:PCT95 12:PCT96 35845 segs, 3290575 residues >US-08-436-265-6 (1-532) from US08436265.pep 53119 segs, 14293498 bases US-08-317-PCT-US94-1 PCT-US94-1 US-08-149-US-08-317summaries Thu May 22 14:32:34 1997; PCT-US95-0 Sequence 5, Application PC/TUS9505467 Sequence 5, Application PC/TUS9505467 PCT-US95-0 US-08-149-SUMMARIES PCT-US94-1 PCT-US94-1 ALIGNMENTS MTQLYIYIRLLGAYLFIISR. Listing first 45 % Query 1506 5 1506 5 1647 10 3238 10 1506 5 Minimum Match 1011 Match Length DB TABLE default not generated. TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: 2076 1952 1506 1506 1813 GENERAL INFORMATION: APPLICANT: APPLICANT: Dbase 0; n-issued PAM 150 Gap 11 3981 Gap 44.2 17.4 . 17.3 8.7 8.7 9 8 8 8 100.0 Query Post-processing: 01-JAN-1900 Tabular output 2932 1296 509 509 255 255 244 241 Perfect Score: Scoring table: .. Scoring table: Score STD Description: XXXXXX Statistics: ch pp Sequence: Searched: Searched: Database Run on: 4201000 Nmatch RESULT Title: SSSSSB48

2.52e-180 1.12e-173 3.45e-171

3.45e-171

Applicatio

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8.06e-183 8.06e-183

Applicatio Applicatio Applicatio Applicatio

0.00e+00 0.00e+00

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Pred. No.

result being printed,

0.00e+00 0.00e+00

scale 0.208 Mean 34.082; Variance 164.028; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Pred. No.	0.00e+00 0.00e+00 0.00e+00 4.14e-231 4.14e-231 6.61e-142 2.78e-140 1.67e-131 8.54e-131 2.37e-130	*
	Application	FIC CELL
Description	Sequence 6, Sequence 4, Sequence 4, Sequence 10, Sequence 17, Sequence 17, Sequence 4, Sequence 6, Sequence 6,	; 532 AA. KOTEIN-SPECI
QI QI	PCT-US95-0 PCT-US94-1 PCT-US94-1 PCT-US94-1 US-08-149- US-08-149- PCT-US94-1 PCT-US95-0 US-08-149-	PCT-US95-05467-6 STANDARD, PRT; 532 AA.  xxxxxxx  01-JAN-1900  Sequence 6, Application PC/TUS9505467.  Sequence 6, Application PC/TUS9505467  APPLICANT: APPLICANT: APPLICANT: TITLE OF INVENTION: SURFACE RECEPTORS AND USES THEREFOR
ength DB	532 11 532 10 502 10 502 11 503 10 501 5 501 5 509 10 509 11	7-6 STANDARD, pplication PC/TUS Application PC/TU ORMATION: : : INVENTION: MORPH INVENTION: SURFA
% Query Match Length	100.0 98.0 69.3 69.3 44.1 44.1 47.1 40.9	T-US95-05467-6 ST  XXXX  -JAN-1900  quence 6, Application equence 6, Application equence Throwarion: APPLICANT: APPLICANT: TITLE OF INVENTION: TITLE OF INVENTION:
Score	3981 3981 2757 2757 1754 1737 1638 1638	PCT-US95-05467-6 XXXXXXX 01-JAN-1900 Sequence 6, Appl Sequence 6, App GENERAL INFORM APPLICANT: APPLICANT: TITLE OF INV
Result No.	1 2 2 4 6 6 7 8 9 0 1	RESULT ID PORTS IN THE PROPERTY IN THE PROPERT

532 AA APPLICANT: GENETICS INSTITUTE, INC. TITLE OF INVENTION: RECEPTOR PROTEINS PRT; Sequence 2, Application PC/TUS9410080 GENERAL INFORMATION: Sequence 2, Application PC/TUS9410080. STANDARD; 19 NUMBER OF SEQUENCES: PCT-US94-10080-2 01-JAN-1900 XXXXXX RESULT 

Gaps 0; Length 532; Query Match 98.0%; Score 3900; DB 10; Best Local Similarity 97.2%; Pred. No. 0.00e+00; 10; Mismatches 517; Conservative Matches

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MasPar time 1709.29 Seconds 1346.573 Million cell updates/sec n.a. - n.a. database search, using Smith-Waterman algorithm Thu Jun 26 00:53:14 1997; MPsrch nn Run on:

Tabular output not generated

>US-08-436-265-13 (1-2070) from US08436265.seq 2070 Description:

Perfect Score: N.A. Sequence:

TABLE default Scoring table:

a-issued 1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93 10:PCT94 11:PCT95 12:PCT96

summaries

Minimum Match 0% Listing first 45

Post-processing:

Database:

Gap

Query 0 Dbase 0; STD Nmatch 333249 segs, 555961234 bases x Searched:

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summaries Minimum Match 0% Post-processing:

Listing first 45

Database:

1:BCT 2:FUN 3:GEN 4:HUM1 5:HUM2 6:HUM3 7:INV1 8:INV2 9:INV3 10:INV4 11:INV5 12:INV6 13:INV7 14:ORG 15:MAM 16:VRI 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC embl-new11

23:VIR1 24:VIR2 genbank97 Database:

60:PLN4 61:PLN5 62:PLN6 63:PLN7 64:PLN8 65:PLN9 66:PLN10 67:PRI1 68:PRI2 69:PRI3 70:PRI4 71:PRI5 72:PRI6 73:PRI7 25:BCT1 26:BCT2 27:BCT3 28:BCT4 29:BCT5 30:BCT6 31:BCT7 32:BCT8 33:BCT9 34:GEN1 35:GEN2 36:HTG 37:INV1 38:INV2 39:INV3 40:INV4 41:INV5 42:INV6 43:INV7 44:INV8 45:INV9 46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3 52:PAT1 53:PAT2 54:PAT3 55:PAT4 56:PHG 57:PLN1 58:PLN2 59:PLN3

94:VRL3 95:VRL4 96:VRL5 97:VRL6 98:VRL7 99:VRL8 100:VRL9 80:PRI14 81:ROD1 82:ROD2 83:ROD3 84:ROD4 85:ROD5 86:ROD6 87:ROD7 88:ROD8 89:STR 90:SYN 91:UNA 92:VRL1 93:VRL2 74:PRI8 75:PRI9 76:PRI10 77:PRI11 78:PRI12 79:PRI13

101:BCT 102:GEN 103:INV1 104:INV2 105:MAM 106:VRT 107:PHG 108:PLN 109:PRI1 110:PRI2 111:ROD 112:SYN genbank-new11

Database:

113:UNA 114:VRL Database:

115:part1 116:part2 u-emb148 97

. Mean 12.028; Variance 5.236; scale 2.297 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	; ;	Fred. No.	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00	0.00e+00		25-NOV-1994			
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	f	GT .	MUSBMPRC	MMU04672	MMIJ 04673	875359	MMALK3A	S74037	RATRALK3	RNRALK3	RATRB4R1	HSALK3A		p mRNA	Mouse mRNA for BMP receptor, complete cds.		
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<sub>9</sub> /o	Query	Match Length UB	95.3	86.7	80.4	79.6	77.2	75.6	75.6	75.6	70.4	68.5		MUSBMPRC	use mRNA	D16250	9577633
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BMP receptor. KEYWORDS SOURCE

Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata, Vertebrata, Eutheria, Rodentia, Sciurognathi, Myomorpha, Muridae, Mus musculus brain, library of K. Nakayama and M. Hosaka, cDNA mRNA, clone mTFR11-45. Mus musculus ORGANISM

1 (bases 1 to 2292)
Suzuki,A., Thies,R.S., Yamaji,N., Song,J.J., Wozney,J., Murakami,K.
and Kung,H. REFERENCE AUTHORS

A truncated bone morphogenetic protein receptor affects dorsal-ventral patterning in the early Xenopus embryo TITLE

91, 10255-10259 (1994) Proc. Natl. Acad. Sci. U.S.A. 95024092 JOURNAL MEDLINE

3, Gaps . m Length 2292, 2; Indels 84; Pred. No. 0.00e+00; Score 1973; DB 0; Mismatches 95.3%; 99.7%; Matches 1993; Conservative Best Local Similarity Query Match

17-SEP-1994 MMU04672 2402 bp mRNA ROD 17-S Mus musculus type I receptor BRK-1 mRNA, complete cds. U04672 ~ DEFINITION RESULT COCUS

9538362 ACCESSION

BRK-1; bone morphogenetic protein receptor kinase-1; full-length receptor protein kinase. KEYWORDS

Mus musculus house mouse ORGANISM SOURCE

Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Chordata; Eukaryotae; mitochondrial eukaryotes; Metazoa; Murinae; Mus.

REFERENCE

1 (bases 1 to 2402)
Koenig, B.B., Cook, J.S., Wolsing, D.H., Ting, J., Tiesman, J.P., Correa, P.E., Olson, C.A., Pecquet, A.L., Ventura, F., Grant, R.A., Chen, G., Wrana, J.L., Massague, J. and Rosenbaum, J.S. AUTHORS

Characterization and cloning of a putative receptor for BMP-2 and BMP-4 from NIH3T3 cells TITLE

Mol. Cell. Biol. 14, 5961-5974 (1994) 2 (bases 1 to 2402) 94344106 MEDLINE JOURNAL REFERENCE

Direct Submission Rosenbaum, J.S. AUTHORS TITLE

Company, Miami Valley Laboratories, P.O. Box 398707, Cincinnati, OH The Procter & Gamble Submitted (22-DEC-1993) Jan S. Rosenbaum, JOURNAL

Length 2402; Score 1795; DB 82; Pred. No. 0.00e+00; 86.7%; 45239-8707, USA Query Match

4 Gaps 4; Indels 10; 0; Mismatches Best Local Similarity 99.3%; Matches 1859; Conservative

18-OCT-1995 ROD гичацКЗА 1599 bp RNA M.musculus ALK-3 mRNA, complete CDS. Z23154 9437868 ß DEFINITION ACCESSION RESULT LOCUS

ALK-3 gene; serine/threonine kinase receptor house mouse. KEYWORDS SOURCE

Eukaryotae, mitochondrial eukaryotes, Metazoa, Chordata, Vertebrata, Eutheria, Rodentia, Sciurognathi, Myomorpha, Muridae, Mus musculus ORGANISM

(bases 1 to 1599) REFERENCE AUTHORS

Submitted (25-JUN-1993) Kohei Miyazono, Ludwig Institute for Cancer Research, Biomedical, Center, Uppsala, S-751 24, Sweden Direct Submission Murinae; Mus. Miyazono, K. JOURNAL TITLE

Dewulf,N., Verschueren,K., Lonnoy,O., Moren,A., Grimsby,S., Vande Spiegle,K., Miyazono,K., Huylebroeck,D. and Ten Dijke,P. Distinct spatial and temporal expression patterns of two type I receptors for bone morphogenetic proteins during mouse (bases 1 to 1599) AUTHORS TITLE

REFERENCE

Endocrinology 136 (6), 2652-2663 (1995) embryogenesis 95269711 MEDLINE JOURNAL

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. 0 Length 1599; Indels o' DB 81; Score 1599; DB 81; Pred. No. 0.00e+00; Mismatches ., Query Match
Best Local Similarity 100.0%;
Matches 1599; Conservative

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Gaps

backbone; RNA; ROD; 2620 BP RESULT 6 ID S74037

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Cancer Research, Uppsala, branch, Biomedical Center, Husargatan 3,
                                                                                                                                                                                              Activin receptor-like kinases: a novel subclass of cell-surface
                                                                            Submitted (06-APR-1993) Peter P ten Dijke, Ludwig Institute for
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ten Dijke,P.P., Ichijo,H.H., Franzen,P.P., Schulz,P.P., Saras,J.J.,
Toyoshima,H.H., Heldin,C.C. and Miyazono,K.K.
Activin receptor-like kinases; Anovel subclass of cell surface
receptors with predicted serine/threonine kinase activity
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Vertebrata, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                            "Molecular cloning of rat bone morphogenetic protein (BMP) type IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shinichiro Oida, Faculty of Dent., Tokyo Medical and Dental
University, Department of Biochemistry; 1-5-45 Yushima, Bunkyo-ku,
Tokyo 113, Japan (Tel:03-3813-6111(ex.5126), Fax:03-5684-8047)
                                                      26-AUG-1996 (Rel. 49, Last updated, Version 1)
bone morphogenetic protein type IA receptor [rats, Wistar, dental
pulp cell line RPC-C2A, mRNA, 2620 nt].
                                                                                                                                                                                                                                                                                                                receptor and its expression during ectopic bone formation induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALK-3 gene; cell surface receptor; serine threonine kinase.
                                                                                                                                                                                                                                                        Takeda K., Oida S., Ichijo H., Iimura T., Maruoka Y., Amagasa T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takeda K., Oida S., Ichijo H., Iimura T., Maruoka Y., Amagasa T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinase; morphogenetic protein receptor; rALK-3; serine/threonine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NID
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0.00e+00 0.00e+00 0.00e+00 0.00e+00

Sequence encoding bon Human Activin recepto

Pred. No 0.00e+00 0.00e+00

Description

Mouse Activin recepto

Mouse BMP type I rece

Bone morphogenetic pr

BRK-1 DNA

0.00e+00 0.00e+00 0.00e+00

Modified bone morphog

Mouse incomplete BMP Human ALK-3 cDNA. Truncated BRK-1.

.....TITGCTTTTTTTGTT 2070

961.959 Million cell updates/sec

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4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Fage 64-66; 101pp; English. A cDNA clone (T28021) codes for full-length mouse bone morphogenetic protein (BMP) type I receptor kinase protein-1 (BRK-1) (R95225), a receptor capable of binding BMP and transducing a signal initiated by the binding. Host cells co-transfected with vectors carrying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assays for bone morphogenetic protein activities - using complex of BMP type I receptor kinase protein and BMP receptor kinase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T28018-20 and T28022-30) express a BMP receptor complex useful for screening cpds. for BMP receptor affinity or for determining the concentration of a BMP receptor ligand in a clinical sample.
          transforming growth factor; TGF; diagnostics; detection; therapy; rheumatoid arthritis; glomerular nephritis; fibrosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type II receptor kinase-3; BRK-3; bone morphogenetic protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-length, incomplete or soluble BMP type I receptor kinase protein cDNA and full-length, incomplete, soluble or truncated BMP type II receptor kinase protein-3 (BRK-3) cDNA (see also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23; Length 2402;
                                                                                                                                                                                                                                                                                                                                              Yamashita H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type I receptor kinase; BRK-1; BMP receptor; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1795; DB 23;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse BMP type I receptor kinase (bRK-1) cDNA.
                                                                                                                                                                                                                                                                                                                                              Franzen P, Heldin C, Miyazono K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                 product= activin receptor-like kinase 3
                                                                                                                                                                                                                                                                                                                                                           WPI, 94-183503/22.
2041 GGTTTTTTTGTTTGCTTTTTTTTTGTT 2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T27228 standard; cDNA; 2402 BP. T27228;
                                                                                                                                                                                                                                                                                                                                                                                                                                      T28021 standard; cDNA; 2402 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1994; US-334178.
05-JUN-1995; US-462467.
(PROC ) PROCTER & GAMBLE CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.7%;
                                                                                                                                               1816..2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                   T28021; . . 31-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                    217..1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11..1609
                                                                                                                                                                                                                                                                     28-MAY-1993; GB-011047.
                                                                                                                                                                                                                                                      08-MAR-1993; GB-004680.
                                                                                                                                                                                                                        .7-NOV-1992; GB-024057
                                                                                                                                                                                                                                       08-MAR-1993; GB-004677.
                                                                                                                                                                                                                                                                                  02-JUL-1993; GB-013763
                                                                                                                                                                                                                                                                                                 03-AUG-1993; GB-016099
                                                                                                                                                                                                                                                                                                                 15-OCT-1993; GB-021344
                                                                                                                                                                                                         17-NOV-1993; G02367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-1995; U14027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2402 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 96-251887/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; R95225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09614579-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosenbaum JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 1859;
                                           Mus musculus
                                                                                                                                                                                            26-MAY-1994.
                                                                                                                                                                             WO9411502-A
                                                                                         ø
                                                                                                                                                                                                                                                                                                                                              Dijke P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sp.
                                                                     5'UTR
                                                                                                                                               3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BRK-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BME
                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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screening; reporter gene; bone morphogenetic protein-antagonist;
                                                                                                                                                                                                                                                                                                                                                                                  used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The truncated
           Bone morphogenetic protein type-I receptor kinase-1 gene.
Mouse, bone morphogenetic protein receptor kinase-1,
bone morphogenetic protein receptor kinase-3; antibody; diagnostic,
bone disorder; osteogenic; bone morphogenetic protein-agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           differentiation in response to BMP. The gene may be inserted in plasmid pJT4, to form plasmid pJT4-JI59F, and co-expressed with a type-II BRK-3 gene to study complex formation between the 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bind or scavenge BMPs. In addition, expression of the BRK-3 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bone morphogenic protein; receptor; serine/threonine kinase; BMP; bone; cartilage; injury; treatment; inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor types. The BRK-3 receptor and antibodies against it may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serine/threonine kinase receptors may be used in compositions to inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncs receptors pref. comprise the ligand binding domain, but not the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compounds for BRK-agonist or -antagonist activity, by monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be used in diagnostic assays for BMP disorders, or in therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1795; DB 20; Length 2402; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence encoding bone morphogenic protein receptor CFK1-23a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   704 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Truncated BMP and serine/threonine kinase receptor proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence encodes mouse bone morphogenetic protein (BMP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             along with a reporter gene under the control of a hormone-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              responsive element in a cell culture may be used to screen
                                                                                                                                                                                                                                                                                                                                                                               isolated bone morphogenic protein receptor kinase protein
                                                                                                                                                                                                                                                                                                                                                                                                                  (ant)agonist of BMP receptor kinase protein transcription Example 4; Page 61-63; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     or is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor type-I kinase-1 (BRK-1), which induces cellular
                                                                                                                                                                                                          'product= Bone morphogenetic protein receptor kinase-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Truncated bone morphogenic protein (BMP) receptors and
                                                                                                                                                                                                                                                                                                                                                                                                   determine if a test cpd. is capable of binding to,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serine/threonine kinase and transmembrane domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used to inhibit the effects of BMP-2 and/or BMP-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEMY ) GENETICS INST INC.
Celeste AJ, Thies RS, Wozney JM, Yamaji N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= Bone morphogenic protein receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     482 C;
                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 48-50; 83pp; English.
                                                                                                              hormone-responsive element; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     676 A;
                                                                                                                                                                                                                                                                                                      (PROC ) PROCTER & GAMBLE CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q83530 standard; DNA; 1813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 1859; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reporter gene expression
                                                                                                                                                                      11..1609
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                                                                                                                                                                                                                                                                                   04-NOV-1994; US-334179.
                                                                                                                                                                                                                                                                                                                          Rosenbaum JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-SEP-1994; U10080.
17-SEP-1993; US-123934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2402 BP;
                                                                                                                                                                                                                                                                30-OCT-1995; U14085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 95-131350/17.
                                                                                                                                                                                                                                                                                                                                         WPI; 96-251762/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; R70237.
                                                                                                                                                                                                                                                                                                                                                              P-PSDB; R96201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus rattus.
                                                                                                                                                                                                                           WO9614412-A2
                                                                                                                                                                                                                                            17-MAY-1996.
                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-1995.
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                                                                                                                                                                                       /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ๙
                                                                                                                                                                                                                                                                                                                       Nohno T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                           drug
                                                                                                                                                   Key
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.....TITGCTTTTTTTGTT 2070
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EST109182 Rattus sp. 0.00e+00
K5301F Fetal heart, L 0.00e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human placenta cDNA 5 8.01e-146
Human placenta cDNA 5 8.01e-146
H. sapiens partial CD 7.28e-138
H. sapiens partial CD 6.02e-130
                                                                                                                            4
                                                                                                                                                                            Thu Jun 26 01:26:17 1997; MasPar time 1317.77 Seconds 1006.977 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.78e-221
8.01e-146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.00e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mc33h08.rl Soares mou 5.03e-22.
zf53c07.rl Soares ret 5.78e-221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MasPar time 70.46 Seconds
839.881 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAGTACTCTACCTTCGTAT.......aAACGAAAAAAAAAAAAAAA
                                                                                                                            Gaps

    n.a. database search, using Smith-Waterman algorithm

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           using Smith-Waterman algorithm
                    recombinant mammalian cells expressing them. Such cells can be delivered in a medium or matrix which partially impedes their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zf53c07.rl Soares ret
Human placenta cDNA 5
                                                                                                                           .
ف
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2c18g04.rl Soares par
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H. sapiens partial cD
H. sapiens partial cD
      are soluble and will be excreted into supernatant by
                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                Score 1538; DB 14; Length 1813;
Pred. No. 0.00e+00;
                                             mobility, thereby localising the cells to a site of bone or cartilage injury.
                                                                        471 T;
                                                                                                                          0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                        439 G;
                                                                                                                                                                                                                                                                                                                                                                        887282 seqs, 320523884 bases x
                                                                                                                                                                                                                                                                      1 ATTCATGAGATGGAAGCATA...
                                                                                                                                                                                                                                          (1-2070) from US08436265.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       >US-08-436-265-13
(1-2070) from US08436265.seq
                                                                        397 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53119 seqs, 14293498 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum Match 0%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sat May 24 07:06:02 1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W39552
MMTEST730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA053838
HSA53838
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HSC2ZA061
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N88732
W34981
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                                                                        506 A;
                                                                                                                                                                                                                                >US-08-436-265-13
                                                                                                                                                                                                                                                                                                                                                  Dbase 0; Query 0
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                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
                                                                                                74.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
38
116
116
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231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
                                                                                                                          Matches 1682; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TABLE default
                                                                                                                                                                                                                                                                                                           TABLE default
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not generated.
                                                                                                                                                                                                      Tabular output not generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263
471
739
739
515
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211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259
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                                                                        1813 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                      EST-STS
                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                         Perfect Score:
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          proteins
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237
231
208
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96
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• 8888888
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n-issued Database:

1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93 10:PCT94 11:PCT95 12:PCT96

scale 1.854 Mean 9.280; Variance 5.006; Statistics

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

			_	_	_	_	4	9	0	o)	2	7
		No.	0.0ce+00	0.00e+00	0.00e+00	0.00e+00	2.46e-174	6.84e-169	6.84e-169	L.14e-169	6.70e-162	6.70e-162
		Pred. No.	0.00		0.00	0.00	2.46	6.84	6.84	1.14	6.70	6.70
			Sequence 1, Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio	Applicatio
		6	Ä	2,	,	ω,	6	4,	4,	7,	7	'n
		Description	Sequence	Sequence 5,	Sequence 7,	Sequence	Sequence 9,	Sequence 4,	Sequence 4,	Sequence	Sequence 2,	Sednence
		ID	PCT-US94-1	PCT-US95-0	PCT-US95-0	PCT-US94-1	PCT-US94-1	US-08-317-	US-08-149-	PCT-US94-1	US-08-149-	US-08-317-
		DB	10	11	77	10	10	ß	Ŋ	10	S	Ŋ
		Match Length DB	1813 10	2932	1952	2076	1794	1506	1506	1647	1506	1506
,/o	Query	Match	74.3	68.5	25.1	24.9	12.5	12.2	12.2	12.2	11.7	11.7
		Score	1538	1417	520	516	259	252	252	253	243	243
	Result	No.	г	73	ю	4	5	9	7	80	თ	10

### ALIGNMENTS

													Gaps	
											313;		6	
											Length 18		Indels	
RESULT 1	PCT-US94-10080-1 STANDARD; DNA; UNC; 1813 BP.	XXXXXX	01-JAN-1900	Sequence 1, Application PC/TUS9410080.	Sequence 1, Application PC/TUS9410080	GENERAL INFORMATION:	APPLICANT: GENETICS INSTITUTE, INC.	TITLE OF INVENTION: RECEPTOR PROTEINS	NUMBER OF SEQUENCES: 19	CORRESPONDENCE ADDRESS:	Query Match 74.3%; Score 1538; DB 10; Length 1813;	Best Local Similarity 94.4%; Pred. No. 0.00e+00;	Matches 1682; Conservative 0; Mismatches 90; Indels 9; Gaps	
RESU	ΠD	AC	DI	DE	ပ္ပ	ပ္ပ	ပ္ပ	ပ္ပ	ပ္ပ	ပ္ပ	Qu	Be	Ma	

4,

# PCT-US95-05467-5 STANDARD; DNA; UNC; 2932 RESULT

Sequence 5, Application PC/TUS9505467 Sequence 5, Application PC/TUS9505467 GENERAL INFORMATION: APPLICANT: 01-JAN-1900 XXXXXX

APPLICANT: CCCCCCEFF

protein - protein database search, using Smith-Waterman algorithm SURFACE RECEPTORS AND USES THEREFOR MORPHOGENIC PROTEIN-SPECIFIC CELL TITLE OF INVENTION: MPsrch\_pp

MasPar time 11.06 Seconds 524.120 Million cell updates/sec Tue Jun 24 17:53:39 1997; Run on:

Tabular output not generated.

1 MTQLYTYIRLLGACLFIISH.....TALRIKKTLAKMVESQDVKI 532 >US-08-436-265-14 (1-532) from US08436265.pep 3986 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

Searched:

Gaps

. 0

Indels

·,

Mismatches

·;

Conservative

532;

Matches

Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 a-geneseq26

19:part19

Mean 36.022; Variance 149.415; scale 0.241 Statistics:

Pred. No. is the number of results predicted by chance to have a score picater than or equal to the score of the result being printed, and is cerived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	* Query Match Length DB	DB	8	Description	Pred. No.
1	3986	100.0		19	R95225	Mouse BMP type I rece 0.00e+00	0.00e+00
2	3986	100.0	532 17	17	R96201	Bone morphogenetic pr	0.00e+00
0	3986	100.0		13	R74343	BRK-1 protein.	0.00e+00
7	3961	4.66		13	R70237	Bone morphogenic prot	0.00e+00
Ŋ	3915	98.2	532	14		Human ALK-3.	0.00e+00
9	3915	98.2	532	10	R55368	Human Activin recepto	
7	3686	92.5	500	13	R74342	Truncated BRK-1.	0.00e+00
ω	2756		502	14	R8520°	Mouse ALK-6.	6.06e-267
0	. 2756	1.69.1	502	13	77.023.B	Bone morphogenic prot	6.06e-267
10	2746	2746 * 68.9	502 19	19	R95226	Chick BMP type I rece	6.56e-266
			ď	LIG	ALIGNMENTS		

Mouse BMF type I receptor kinase protein (BRK-1). BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein; BMP type I receptor kinase; BRK-1; BMP receptor. R95225 standard; Protein; 532 AA. (first entry) 31-DEC-1996 R95225; gb. Mus AESULT
AS AC R9
AC R9
DD 31
DD R0
DD R0
EW BM
KW BM
KW BM
KW BM
COS MU
DP DO 17
PP 30
PP 30
PP 30
PP 30

17-MAY-1996. 30-OCT-1995; U14027. W09614579-A1.

04-NOV-1994; US-334178. 05-JUN-1995; US-462467. (PROC ) PROCTER & GAMBLE CO. Rosenbaum JS;

Assays for bone morphogenetic protein activities - using complex of BMP type I receptor kinase protein and BMP receptor kinase protein WPI; 96-251887/25. N-PSDB; T95225.

using complex of

Full-length mouse borearghogenetic protein (BMP) type I receptor kinase protein-1 (BRK-1) (R95225) is a receptor capable of binding BMP and transducing a signal initiated by the binding. Its amino acid sequence was deduced from a cDNA clone (T28021). A BMP receptor kinase protein complex formed of full-length, incomplete or soluble BMP type I receptor kinase protein and full-length, incomplete or soluble BMP type II receptor kinase also R95222-24 and R95226-34) is useful for screening cpds. For BMP Claim 2; Page 66-67; 101pp; English. 

receptor affinity or for determining the concentration of a BMP receptor ligand in a clinical sample. The complex can be expressed by host cells co-transfected with vectors carrying the appropriate DNA sequences (see also T28018-30).

o;

Sequence

Length 532; Score 3986; DB 19; Pred. No. 0.00e+00; Query Match Best Local Similarity 100.0%;

New bone morphogenetic protein receptor kinase protein - used for identifying cpds. capable of binding it and for developing therapeutic drug screening; reporter gene; bone morphogenetic protein-antagonist; Gaps bone morphogenetic protein receptor kinase-3; antibody; diagnostic; bone disorder; osteogenic; bone morphogenetic protein-agonist; Vectors including the DNA were used to express recombinant BRK-1 in cpds. and detection system(s)
Claim 1, Page 29-32, 49pp, English.
A cDNA library prepared from NIH3T3 poly-A RNA was screened with
J159 PCR fragment to isolate clone BRK-1 (sequence given in
Q90184) encoding full-length BMP receptor kinase protein (R74343) Bone morphogenic protein receptor CFK1-23a. Bone morphogenic protein; receptor; serine/threonine kinase; BMP; BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein. 0; Length 532; Indels Ting J; Mouse; bone morphogenetic protein receptor kinase-1; Bone morphogenetic protein type-I receptor kinase-1. . 0 Score 3986; DB 13; Pred. No. 0.00e+00; Rosenbaum JS, 0; Mismatches /label= Extracellular\_ligand\_binding\_domain Domain 153..176 'note= "Peptide used to raise antibody" Location/Qualifiers Location/Qualifiers /label= Intracellular\_kinase\_domain Correa PE, Koenig BB, J. 3 R74343 standard; Protein; 532 AA. 532 AA 'note= "Conserved BRK-1 motif" R96201 standard; Protein; 532 /label= Transmembrane domain 8 24-NOV-1993; US-158735. (PROC ) PROCTER & GAMBLE CO. Query Match Best Local Similarity 100.0%; hormone-responsive element (first entry) 28-SEP-1995 (first entry) (first entry) JT 4 R70237 standard; Protein; (PROC ) PROCTER & GAMBLE Nohno I, Rosenbaum JS; 532; Conservative 216..221 24..152 04-NOV-1994; US-334179. 1..23 CHO and COS-7 hosts. 23-NOV-1994; U13534. 30-OCT-1995; U14085 /label= Sig\_peptide WPI; 95-206935/27. N-PSDB; Q90184. BKK-1 protein. WO9614412-A2. 22-AUG-1996 Mus musculus 17-MAY-1996. 01-NOV-1995 W09514778-A. 01-JUN-1995 Cook JS, Sequence Peptide R96201; Peptide R74343; R70237; Mus sp. Peptide Domain Domain Domain Matches Key RESULT RESULT ID AC DI

cycsghcpddainntcitnghcfaiieeddggettlasgcmkyegsdfgckdspkaglrr 120 in the design of morphogen agonists and antagonists for therapeutic, diagnostic and experimental purposes 1 MTQLYTYIRLLGACLFIISHVQGQNLDSMLHGTGMKSDLDQKKPENGVTLAPEDTLPFLK gkgrygevwmgkwrgekvavkvfftteeaswfreteiyqtv1mrheni1gfiaadikgtg GKGRYGEVWMGKWRGEKVAVKVFFTTEEASWFRETEIYQTVLMRHENILGFIAADIKGTG Swtglylitdyhengslydflkcatldtrallklaysaacglchlhteiygtggkpaiah 1 mtqlyiyirllgaylfiisrvqgqnldsmlhgtgmksdsdqkksengvtlapedtlpflk ALK-3; OP1 binding receptor; osteogenic protein 1; morphogenesis; The Type-I cell surface receptors ALK-2, ALK-3 and ALK-6 (given R85206, R85207 and R85209) have specific binding affinity for osteogenic protein 1 (OP1) and OP1-related analogues. The receptors are used to identify novel morphogen receptor binding Identifying osteogenic protein-1 receptor-binding analogue pivsnrwnsdeclravlklmsecwahnpasrltalrikktlakmvesgdvki 4; Indels Score 3915; DB 14; Pred. No. 0.00e+00; Ϋ́ 6; Mismatches Sampath Location/Qualifiers Claim 1, Page 68-71, 95pg English. Dijke PT, Heldin C, Miyazano K, 29-APR-1994; US-236428. (CREA-) CREATIVE BIOMOLECULES INC /label= Intracellular\_domain /note= "serine/threonine-kinase analogues useful in drug design. (LUDW-) LUDWIG INST CANCER RES. morphogen; agonist; antagonist /label= Extracellular domain Domain 153..235 /label= Transmembrane\_domain Domain 236..527 Query Match Best Local Similarity 98.1%; 522; Conservative 24..152 28-APR-1995; U05467 peptide WPI; 95-393076/50. 532 AA; N-PSDB; T06031 WO9530003-A2. 09-NOV-1995. Homo sapiens /label= Sig Sequence Peptide Domain Domain Domain Matches 61 61 421 241 241 301 301 361 361 421 481 원 g ò ò 원 ò g ò 임 à d à g g ò à ô 180 240 240 61 CYCSGHCPDDAINNTCITNGHCFAIIEEDDQGETTLISGCMKYEGSDFQCKDSPKAQLRR 120 480 Claim 16, Page 50-51, 83pp, English.

Truncated bone morphogenic protein (BMP) receptors and serine/threonine kinase receptors may be used in compositions to inhibit the effects of BMP's such as BMP-2 and BMP-4. The truncated receptors pref. comprise the ligand binding domain, but not the serine/threonine kinase and transmembrane domains. The truncated proteins are soluble and will be excreted into supernatant by 61 cycsghcpddainntcitnghcfaiieeddqgettltsgcmkyegsdfqckdspkaqlrr 120 tieccrtnlcngylgptlppvvigpffdgsvrwlavlismavcivamivfsscfcykhyc 180 9 Gaps 121 TIECCRINICNQYLQPTLPPVVIGPFFDGSIRWLVVLISMAVCIVAMIIFSSCFCYKHYC ksissrgrynrdlegdeafipvges1kdlidgsgssgsgsg1p11vgrtiakgigmvrqv rdlksknilikkngscciadlglavkfnsdtnevdiplntrvgtrrymapevldeslskn hfqpyimadiysfglliwemarrcitggiveeyqlpyynmvpsdpsyedmrevvcvkrlr KSISSRGRYNRDLEQDEAFIPVGESLKDLIDQSQSSGSGSGLPLLVQRTIAKQIQMVRQV 421 HFQPYIMADIYSFGLIIWEMARRCITGGIVEEYQLPYYNWVPSDPSYEDMREVVCVKRLR recombinant mammalian cells expressing them. Such cells can be ; 0 delivered in a medium or matrix which partially impedes their Truncated BMP and serine/threonine kinase receptor proteins 99.4%; Score 3961; DB 13; Length 532; 98.9%; Pred. No. 0.00e+00; mobility, thereby localising the cells to a site of bone or pivsnrwnsdeclravlklmsecwahnpasrltalrikktlakmvesgdvki 1; Indels used to inhibit the effects of BMP-2 and/or BMP-4. cartilage; injury; treatment; inhibition 5; Mismatches Celeste AJ, Thies RS, Wozney JM, WPI; 95-131350/17. Ā LT 5 R85207 standard, Protein, R85207; (GEMY ) GENETICS INST INC. 526; . Conservative 07-SEP-1994; U10080. 17-SEP-1993; US-123934. Best Local Similarity 532 AA; cartilage injury N-PSDB; Q83530. Rattus rattus. WO9507982-A. 13-FEB-1996 Human ALK-3. 23-MAR-1995 Sequence Query Match 181 361 481 121 181 361 421 Matches RESULT
ID R8
AC R8
DT 13
DE Hu S C ò ď õ J. ò g  $\delta$ à 엄 à В à g ò qq ; marinet with the 机砂锅

Frengass

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Gaps

0;

Length 532;

240

240 300 300 360 420

420 480 480

# 481 PIVSNRWNSDECLRAVLKLMSECWAHNPASRLTALRIKKTLAKMVESQDVKI 532

protein - protein database search, using Smith-Waterman algorithm MPsrch\_pp

ن. ن

H.; Heldin,

#authors

REFERENCE

781.251 Million cell updates/sec MasPar time 19.41 Seconds Tue Jun 24 17:52:10 1997; Run on:

Fabular output not generated

(1-532) from US08436265.pep >US-08-436-265-14 Description:

1 MTQLYTYIRLLGACLFIISH.....TALRIKKTLAKMVESQDVKI 532 3986 Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

89912 segs, 28507787 residues Searched:

summaries Listing first 45 Minimum Match 0% Post-processing:

Database:

1:annl 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8

13:unann9 14:unann10 15:unenc 16:unrev

Mean 48.972; Variance 115.254; scale 0.425 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		٥			SOUTHWINES		
Result		Query					
No.	Score	Match	Match Length	DB	ΠD	Description	Pred. No.
r-1	3986	0.0014- 986	532	14	A56238	bone morphogenetic p	0.00e+00
N	3962.5	99.4		14	JC2387	bone morphogenetic p	0.00e+00
m	3915	. 98.2	532	13	S37183		0.00e+00
7	3915	98.2		13	137163	ALK-3 - human	0.00e+00
Ŋ	3686	92.5		14	B56238	bone morphogenetic p	0.00e+00
9	3124	78.4		12	A54985	BMP receptor precurs	0.00e+00
7	2756	69.1		14	A53444	activin receptor-lik	0.00e+00
60	2756	69.1	502	14	JC2491	serine/threonine kin	0.00e+00
Q	2746	68.8		13	A56683	receptor protein kin	0.00e+00
10	1770	44.4	503	13	A49432	activin receptor-lik	1.52e-283
11	1763	44.2	503	14	JC2061	transforming growth	2.75e-282
					ALIGNMENTS		
RESILT	1						
ENTRY	ı	A56238	238	#ty	#type complete		
TTTLE		bone	e morroh	gen	etic protein	bone morphogenetic protein receptor BRK-1 - mouse	
ALTERNATE NAMES	TE NAME		-3 prot	ein;	ALK-3 protein; BMP receptor		
ORGANISM	Į		rmal na	ne M	ns musculus #	#formal name Mus musculus #common name house mouse	v
DATE		03-(	03-Oct-1995	s# 9	equence_revis	#sequence_revision 03-Oct-1995 #text_change	change
		ŏ	06-Sep-1996	966			
ACCESSIONS	SNO	A56.	A56238; S40158;	0158	148242;	I49543	
REFERENCE	Œ	A56238	238				
#ant	#authors	Koeı	nig, B.l	., m	Cook, J.S.; W	Koenig, B.B.; Cook, J.S.; Wolsing, D.H.; Ting, J.; Tiesman,	; Tiesman,
		ט	.P.; Co:	rrea	, P.E.; Olson	J.P.; Correa, P.E.; Olson, C.A.; Pecquet, A.L.; Ventura,	Ventura,
		124	.; Gran	r, R	.A.; Chen, G.	F.; Grant, R.A.; Chen, G.X.; Wrana, J.L.; Massague,	gue, J.;
		×	Rosenbaum, J.S.	٦, ص	s.		
#journal	rnal	Mol	. Cell.	Bio	Mol. Cell. Biol. (1994) 14:5961-5974	5961-5974	
#title	le	Cha	Characterization	zati	and	a receptor for	BMP-2 and
:	-	BMP	BMP-4 from NIH	Z E	IH 3T3 cells.		

1-532 ##label KOE

##cross-references GB:U04672

##residues

##molecule\_type mRNA##molecule\_type mRNA##molecule\_type mRNA##molecule\_type mRNA##molecule\_type

A56238

#accession

```
Distinct spatial and temporal expression patterns of two type I receptors for bone morphogenetic proteins during mouse
                                                                                                                                                                                                                                                                        Dewulf, N.; Verschueren, K.; Lonnoy, O.; Moren, A.; Grimsby, S.; Vande Spiegle, K.; Miyazono, K.; Huylebroeck, D.; Ten Dijke, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suzuki, A.; Thies, R.S.; Yamaji, N.; Song, J.J.; Wozney, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oʻ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #domain signal sequence #status predicted #label SIG\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takeda, K.; Oida, S.; Ichijo, H.; Iimura, T.; Maruoka, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #domain signal sequence #status predicted #label SIG\
#product bone morphogenetic protein type IA receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type IA receptor and its expression during ectopic bone formation induced by BMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A truncated bone morphogenetic protein receptor affects dorsal-ventral patterning in the early Xenopus embryc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Rattus norvegicus #common_name Norway rat 20-Feb-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #checksum 6896
                                          ten Dijke, P. submitted to the EMBL Data Library, June 1993 ALK-3 and ALK-6: the closely related members in the serine/threonine kinase receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular cloning of rat bone morphogenetic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. (1994) 91:10255-10259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ##cross-references EMBL:Z23154; NID:g437868; CDS_PID:g437869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bone morphogenetic protein type IA receptor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. (1994) 204:203-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #label KIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross-references GB:D16250; NID:g577633; CDS_PID:g577634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary; translated from GB/EMBL/DDBJ
S40158
Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo,
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Pred. No. 0.00e+00;
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Activin receptor-like kinases; Anovel subclass of cell
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                                                                                                                                                                                                                                                                                                                                                       surface receptors with predicted serine/threonine kinase
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Characterization and cloning of a receptor for BMP-2
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frog
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                                                                                                                        J.J.; Celeste, A.J.; Melton,
                                                                                                                                                                                                  mesoderm-inducing signals override dorsal signals in vivo.
                                                                                                                                                                                                                                          preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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BMP receptor precursor - African clawed frog
#formal_name Xenopus laevis #common_name African clawed
11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activin receptor-like kinase 6 precursor - mouse #formal name Mus musculus #common name house mouse 19-May-1994 #sequence_revision 19-May-1994 #text_change 08-Dec-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 RGRYNRDIEQDEAFIPVGESLKDLIDQSQSSGSGGLPLLVQRTIAKQIQMYRQVGKGRY
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 527;
                                                                                                                                                                                                                                                                                                                                                           #domain protein kinase homology #label KIN #length 527 #molecular-weight 59800 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                    not given
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                          55; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.4%; Score 3124; DB 12; Best Local Similarity 79.9%; Pred. No. 0.00e+00;
                                                                                                                      Song,
                                                                                                                                                                                                                                                                                                    .
S
                                                                                                                                                                                                                                                                                                                     #superfamily protein kinase
                                                                                                                                                                              Studies with a Xenopus BMP
                                                                                                                      Graff, J.M.; Thies, R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #type complete
                                                                                                                                                                                                                                                                                                  nucleotide sequence
                                                                                                                                                             Cell (1994) 79:169-179
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60 DDSGTPVVTSGCLGLEGSDFQCRDTPIPHQRRSIECCTERNECNKDLHPTLPPLKDRDFV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 MLHGTGMKSDLDQKKPENGVTLAPEDTLPFLKCYCSGHCPDDAINNTCITNGHCFAIIEE
 Sequence 17, Applicati
Sequence 6, Applicatio
Sequence 4, Applicatio
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                                            Sequence 14, Applicati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MORPHOGENIC PROTEIN-SPECIFIC CELL SURFACE RECEPTORS AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 502;
                                                                                                                                                                                                                                                                                                                                                                    Length 532,
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                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genetics Institute Inc. - Legal Affairs
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72.1%; Pred. No. 4.94e-232;
7ative 74; Mismatches 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          532
                                                                                                      532
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                                                                                                                                                                                                                                                                  RECEPTOR PROTEINS
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                                                                                                      PRT;
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             PCT-US94-1
PCT-US95-0
                                                                                                                                                                                                                      Sequence 2, Application Ft, 1359416680
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GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application PC/TUS9410080 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application PC/TUS9505467.
                                           US-08-149-
                                                                                                                                                                                                                                                                                                                     STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application PC/TUS9410080.
  US-08-317-
                                                                                                                                                                                          Sequence 2, Application PC/TUS9410080
                                                         ALIGNMENTS
                                                                                                                                                                                                                                                   GENETICS INSTITUTE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GENETICS INSTITUTE, TITLE OF INVENTION: RECEPTOR P.
                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                      STANDARD;
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Best Local Similarity 98.9%;
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
  501
509
509
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                                                                                                                                                                                                                                     GENERAL INFORMATION
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PCT-US94-10080-4
 43.8
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                                                                                                                                                                           Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.;
A53444
ten Dijke, P.; Yamashita, H.; Ichijo, H.; Franzen, P.; Laiho,
M.; Miyazono, K.; Heldin, C.H.
Science (1994) 264:101-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.94e-232
4.94e-232
3.14e-143
1.03e-141
                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein - protein database search, using Smith-Waterman algorithm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.00e+00
0.00e+00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MTQLYTYIRLEGACLFIISH.....TALRIKKTLAKMVESQDVKI 532
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                         Characterization of type I receptors for transforming
                                                                                                                                                                                                                                                                                                                                                                    #length 502 #molecular-walgint 56944 #checksum 5099
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Sequence 6, Applicatio
Sequence 4, Applicatio
Sequence 8, Applicatio
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Sequence 17, Applicati
                                                                                                                                                                                                     submitted to the EMBL Data Library, June 1993 ALK-3 and ALK-6: the Chusty related members in serine/threonine kinase receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                 DB 14; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                     #domain protein kiness homology #label KIN
                                                                                                                                                                                                                                                                                                                                                                                                                            76; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scale 0.209
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                                                                                                                                                                                                                                                                                                                       #superfamily protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mean 33.987; Variance 162.888;
                                                                                                                                                                                                                                                                                                                                                                                               Score 2756;
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(1-532) from US08436265.pep
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PCT-US95-0
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US-08-149-
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                                                                        factor-beta and activin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                             ##residues 1-502 ##label TEN ##cross-references GB:Z23143
                                                                                                                                                                                                                                                                                          1-502 ##label MIY
                                                                                                                                                                                                                                                                                                           ##cross-references EMBL: Z23143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum Match 0%
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                                                                                                                                                                                                                                                                                                                                                                                              tch 69.1%;
al Similarity 72.1%;
364; Conservative
                                                                                                                                                                                          ten Dijke, P.
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Match Length
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Run on:

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